DOCUMENT-IDENTIFIER: US 6280950 B1
TITLE: Nucleic acid affinity columns

DEPR:
The affinity matrix can also be used to capture (isolate) and thereby purify unknown nucleic acid sequences. For example, an affinity matrix can be prepared that contains nucleic acid (affinity ligands) that are complementary to sequences not previously identified, or not previously known to be expressed in a particular nucleic acid sample. The sample is then hybridized to the affinity matrix and those sequences that are retained on the affinity matrix are "unknown" nucleic acids. The retained nucleic acids can be eluted from the matrix (e.g. at increased temperature, increased destabilizing agent concentration, or decreased salt) and the nucleic acids can then be sequenced according to standard methods.

DOCUMENT-IDENTIFIER: US 6280935 B1
TITLE: Method of detecting the presence or absence of a plurality of target
sequences using oligonucleotide tags

DEPR:
A panning step may be implemented by providing a sample of tag-cDNA conjugates each of which contains a capture moiety at an end opposite, or distal to, the oligonucleotide tag. Preferably, the capture moiety is of a type which can be released from the tag-cDNA conjugates, so that the tag-cDNA conjugates can be sequenced with a single-base sequencing method. Such moieties may comprise biotin, digoxigenin, or like ligands, a triplex binding region, or the like. Preferably, such a capture moiety comprises a biotin component. Biotin may be attached to tag-cDNA conjugates by a number of standard techniques. If appropriate adapters containing PCR primer binding sites are attached to tag-cDNA conjugates, biotin may be attached by using a biotinylated primer in an amplification after sampling. Alternatively, if the tag-cDNA conjugates are inserts of cloning vectors, biotin may be attached after excising the tag-cDNA conjugates by digestion with an appropriate restriction enzyme followed by isolation and filling in a protruding strand distal to the tags with a DNA polymerase in the presence of biotinylated uridine triphosphate.

Detection of **BCR**-ABL transcripts in chronic myeloid **leukemia** (CML) using a 'real time' quantitative RT-**PCR** assay.

AU Preudhomme C; Revillion F; Merlat A; Hornez L; Roumier C; Duflos-Grardel N; Jouet J P; Cosson A; Peyrat J P; Fenaux P

CS Laboratoire d'Hematologie A, Hopital Calmette, Centre Hospitalier Universitaire, Unite Inserm U524, Lille, France.

SO LEUKEMIA, (1999 Jun) 13 (6) 957-64.
Journal code: LEU; 8704895. ISSN: 0887-6924.

CY ENGLAND: United Kingdom

DT Journal; Article; (JO

PubMed ID: 10482989

TI Monitoring of **BCR**-ABL expression using real-time RT-**PCR** in CML after bone marrow or peripheral blood stem cell transplantation.

AU Eder M; Battmer K; Kafert S; Stucki A; Ganser A; Hertenstein B

CS Medizinische Hochschule Hannover, Abteilung Hamatologie und Onkologie, Zentrum der Inneren Medizin, Germany.

SO LEUKEMIA, (1999 Sep) 13 (9) 1383-9.
Journal code: LEU; 8704895. ISSN: 0887-6924.

CY ENGLAND: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)

LA English

ANSWER 17 OF 34 MEDLINE DUPLICATE 11

AN 1998387760 MEDLINE

DN 98387760 PubMed ID: 9722305

TI Quantitation of minimal residual disease in Philadelphia chromosome positive chronic myeloid leukaemia patients using real-time quantitative RT-**PCR**.

AU Mensink E; van de Locht A; Schattenberg A; Linders E; Schaap N; Geurts van Kessel A; De Witte T

CS Department of Haematology, University Hospital Nijmegen, The Netherlands.

SO BRITISH JOURNAL OF HAEMATOLOGY, (1998 Aug) 102 (3) 768-74.
Journal code: AXC; 0372544. ISSN: 0007-1048.

CY ENGLAND: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 199810

ED Entered STN: 19981020
Last Updated on STN: 19981020
Entered Medline: 19981007

L7 ANSWER 9 OF 21 CAPLUS COPYRIGHT 2002 ACS
AN 1997:267258 CAPLUS
DN 126:248579
TI Diagnosis and monitoring of chronic myelogenous leukemia by detection of bcr2-abl2 and bcr3-abl2 translocations
IN Brown, Janice; Lockhart-Bruce, Connie
PA Dade International Inc., USA
SO PCT Int. Appl., 79 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9708339	A1	19970306	WO 1995-US10919	19950828
	W: AU, CA, JP				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	AU 9534178	A1	19970319	AU 1995-34178	19950828
PRAI	US 1995-296258		19950825		
	WO 1995-US10919		19950828		

AB Methods are provided for conducting chronic myelogenous leukemia (CML) assays to detect or monitor CML cells in a human patient. A sample is obtained from the patient and total RNA is extd. The extd. RNA is contacted with appropriate primers that surround the bcr2-abl2 or the bcr3-abl2 translocation regions of the Philadelphia chromosome, and the inter-primer regions are amplified. After amplification, the reaction product, if any, is captured onto a solid phase by means of a capture agent and is detected by means of a labeled detector agent. The amt. of labeled detector agent is correlated with the presence or quantity of CML cells in the patient.

L2 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2002 ACS
AN 1988:543577 CAPLUS
DN 109:143577
TI The bcr genes and transcripts
AU Lifshitz, B.; Fainstein, E.; Marcelle, C.; Shtivelman, E.; Amson, R.; Gale, R. P.; Canaani, E.
CS Dep. Chem. Immunol., Weizmann Inst. Sci., Rehovot, 76100, Israel
SO Oncogene (1988), 2(2), 113-17
CODEN: ONCNES; ISSN: 0950-9232
DT Journal
LA English
AB Human chronic myelogenous leukemia (CML) is a clonal hematol. disorder. CML is characterized by the t(9:22) chromosome translocation which results in translocation of the oncogene abl from chromosome 9 into the breakpoint cluster region (bcr) gene on chromosome 22. The cDNA of the normal bcr gene was cloned and characterized. The bcr gene codes for a protein of 1271 amino acids. The open reading frame is preceded by a region high in GC. At the 5' of this region several GC motifs were identified which are probably involved in the initiation of bcr transcription. The bcr transcripts of 7.0 and 4.5 kb are expressed in all cell types examd. These transcripts share all cDNA sequences analyzed, including the 5' untranslated region. The latter as well as 902 or 927 amino acids are included within the CML-specific bcr-abl mRNA transcribed from the chimeric bcr-abl gene on chromosome 22. In addn. to the complete bcr gene, the human genome contains 3 bcr-related genes contg. the last 7 exons of the intact bcr gene. One of these genes was analyzed in detail and showed higher sequence homol. with the latter. The 3 bcr-related genes were probably derived from the intact gene by subsequent steps of duplication.

ANSWER 22 OF 34 MEDLINE DUPLICATE 13
AN 96203831 MEDLINE
DN 96203831 PubMed ID: 8630427
TI Comparison of genomic DNA and cDNA for detection of residual disease after treatment of chronic myeloid **leukemia** with allogeneic bone marrow transplantation.
AU Zhang J G; Lin F; Chase A; Goldman J M; Cross N C
CS LRF Leukaemia Unit, Royal Postgraduate Medical School, Hammersmith Hospital, London, UK.
SO BLOOD, (1996 Mar 15) 87 (6) 2588-93.
Journal code: A8G; 7603509. ISSN: 0006-4971.
CY United States
DT Journal; Artic